

## SEQUENCE LISTING

## 5 (1) GENERAL INFORMATION:

- 10 (i) APPLICANTS: Kendall, Richard L.  
Thomas, Kenneth A.  
Mao, Xianzhi  
Tebben, Andrew J.
- (ii) TITLE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE, KDR
- 15 (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:  
20 (A) ADDRESSEE: Merck & Co., Inc.  
(B) STREET: P.O. Box 2000  
(C) CITY: Rahway  
(D) STATE: NJ  
(E) COUNTRY: US  
(F) ZIP: 07065-0907
- 25 (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- 30 (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:
- 35 (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Hand, J. Mark  
(B) REGISTRATION NUMBER: 36,545  
(C) REFERENCE/DOCKET NUMBER: 19963PV
- 40 (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 732/594-3905  
(B) TELEFAX: 732/594-4720

## 45 (2) INFORMATION FOR SEQ ID NO:1:

- 50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4071 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGAGAGCA AGGTGCTGCT GGCCGTCGCC CTGTGGCTCT GCGTGAGAC CCGGGCCGCC 60  
 5 TCTGTGGGTT TGCCTAGTGT TTCTCTTGAT CTGCCCAGGC TCAGCATACA AAAAGACATA 120  
 CTTACAATTA AGGCTAATAC AACTCTTCAA ATTACTTGCA GGGGACAGAG GGACTTGGAC 180  
 10 TGGCTTTGGC CCAATAATCA GAGTGGCAGT GAGCAAAGGG TGGAGGTGAC TGAGTGCAGC 240  
 GATGGCCTCT TCTGTAAGAC ACTCACAATT CCAAAAGTGA TCGGAAATGA CACTGGAGCC 300  
 TACAAGTGCT TCTACCGGGA AACTGACTTG GCCTCGGTCA TTTATGTCTA TGTTCAAGAT 360  
 15 TACAGATCTC CATTTATTGC TTCTGTTAGT GACCAACATG GAGTCGTGTA CATTACTGAG 420  
 AACAAAAACA AAAGTGTGGT GATTCCATGT CTCGGGTCCA TTTCAAATCT CAACGTGTCA 480  
 20 CTTTGTGCAA GATACCCAGA AAAGAGATTT GTTCCTGATG GTAACAGAAT TTCCTGGGAC 540  
 AGCAAGAAGG GCTTTACTAT TCCCAGCTAC ATGATCAGCT ATGCTGGCAT GGTCTTCTGT 600  
 GAAGCAAAAA TTAATGATGA AAGTTACCAG TCTATTATGT ACATAGTTGT CGTTGTAGGG 660  
 25 TATAGGATTT ATGATGTGGT TCTGAGTCCG TCTCATGGAA TTGAACTATC TGTTGGAGAA 720  
 AAGCTTGTCT TAAATTGTAC AGCAAGAACT GAACTAAATG TGGGGATTGA CTTCAACTGG 780  
 30 GAATACCCCTT CTTGGAAGCA TCAGCATAAG AAAGTTGTAA ACCGAGACCT AAAAACCAG 840  
 TCTGGGAGTG AGATGAAGAA ATTTTGTGAGC ACCTTAACTA TAGATGGTGT AACCCGGAGT 900  
 GACCAAGGAT TGTACACCTG TGCAGCATCC AGTGGGCTGA TGACCAAGAA GAACAGCACA 960  
 35 TTTGTCAGGG TCCATGAAAA ACCTTTTGTG GCTTTTGGAA GTGGCATGGA ATCTCTGGTG 1020  
 GAAGCCACGG TGGGGGAGCG TGTCAGAATC CCTGCGAAGT ACCTTGGTTA CCCACCCCCA 1080  
 40 GAAATAAAAT GGTATAAAAA TGGAATACCC CTTGAGTCCA ATCACACAAT TAAAGCGGGG 1140  
 CATGTACTGA CGATTATGGA AGTGAGTGAA AGAGACACAG GAAATTACAC TGTCATCCTT 1200  
 ACCAATCCCA TTTCAAAGGA GAAGCAGAGC CATGTGGTCT CTCTGGTTGT GTATGTCCCA 1260  
 45 CCCCAGATTG GTGAGAAATC TCTAATCTCT CCTGTGGATT CCTACAGTA CGGCACCACT 1320  
 CAAACGCTGA CATGTACGGT CTATGCCATT CCTCCCCGC ATCACATCCA CTGGTATTGG 1380  
 50 CAGTTGGAGG AAGAGTGC GC CAACGAGCCC AGCCAAGCTG TCTCAGTGAC AAACCCATAC 1440  
 CCTTGTGAAG AATGGAGAAG TGTGGAGGAC TTCCAGGGAG GAAATAAAAT TGAAGTTAAT 1500  
 AAAATCAAT TTGCTCTAAT TGAAGGAAAA AACAAAAGTG TAAGTACCCT TGTTATCCAA 1560  
 55 GCGGCAAATG TGTCAGCTTT GTACAAATGT GAAGCGGTCA ACAAAGTCGG GAGAGGAGAG 1620  
 AGGGTGATCT CCTTCCACGT GACCAGGGGT CCTGAAATTA CTTTGCAACC TGACATGCAG 1680

	CCCACTGAGC	AGGAGAGCGT	GTCTTTGTGG	TGCACTGCAG	ACAGATCTAC	GTTTGAGAAC	1740
	CTCACATGGT	ACAAGCTTGG	CCCACAGCCT	CTGCCAATCC	ATGTGGGAGA	GTTGCCCACA	1800
5	CCTGTTTGCA	AGAACTTGGA	TACTCTTTGG	AAATTGAATG	CCACCATGTT	CTCTAATAGC	1860
	ACAAATGACA	TTTTGATCAT	GGAGCTTAAG	AATGCATCCT	TGCAGGACCA	AGGAGACTAT	1920
10	GTCTGCCTTG	CTCAAGACAG	GAAGACCAAG	AAAAGACATT	GCGTGGTCAG	GCAGCTCACA	1980
	GTCCTAGAGC	GTGTGGCACC	CACGATCACA	GGAAACCTGG	AGAATCAGAC	GACAAGTATT	2040
	GGGGAAGCA	TCGAAGTCTC	ATGCACGGCA	TCTGGGAATC	CCCCTCCACA	GATCATGTGG	2100
15	TTTAAAGATA	ATGAGACCCT	TGTAGAAGAC	TCAGGCATTG	TATTGAAGGA	TGGGAACCGG	2160
	AACCTCACTA	TCCGCAGAGT	GAGGAAGGAG	GACGAAGGCC	TCTACACCTG	CCAGGCATGC	2220
20	AGTGTTCCTG	GCTGTGCAAA	AGTGGAGGCA	TTTTTCATAA	TAGAAGGTGC	CCAGGAAAAG	2280
	ACGAACTTGG	AAATCATTAT	TCTAGTAGGC	ACGGCGGTGA	TTGCCATGTT	CTTCTGGCTA	2340
	CTTCTTGTC	TCATCCTACG	GACCGTTAAG	CGGGCCAATG	GAGGGGAACT	GAAGACAGGG	2400
25	TACCTGTCCA	TCGTCATGGA	TCCAGATGAA	CTCCCATTTG	ATGAACATTG	TGAACGACTG	2460
	CCTTATGATG	CCAGCAAATG	GGAATTCCTC	AGAGACCGGC	TGAAGCTAGG	TAAGCCTCTT	2520
30	GGCCGTGGTG	CCTTTGGCCA	AGTGATTGAA	GCAGATGCCT	TTGGAATTGA	CAAGACAGCA	2580
	ACTTGCAGGA	CAGTAGCAGT	CAAAATGTTG	AAAGAAGGAG	CAACACACAG	TGAGCATCGA	2640
	GCTCTCATGT	CTGAACTCAA	GATCCTCATT	CATATTGGTC	ACCATCTCAA	TGTGGTCAAC	2700
35	CTTCTAGGTG	CCTGTACCAA	GCCAGGAGGG	CCACTCATGG	TGATTGTGGA	ATTCTGCAAA	2760
	TTTGAAACC	TGTCCACTTA	CCTGAGGAGC	AAGAGAAATG	AATTTGTCCC	CTACAAGACC	2820
40	AAAGGGGCAC	GATTCCGTCA	AGGGAAAGAC	TACGTTGGAG	CAATCCCTGT	GGATCTGAAA	2880
	CGGCGCTTGG	ACAGCATCAC	CAGTAGCCAG	AGCTCAGCCA	GCTCTGGATT	TGTGGAGGAG	2940
	AAGTCCCTCA	GTGATGTAGA	AGAAGAGGAA	GCTCCTGAAG	ATCTGTATAA	GGACTTCCTG	3000
45	ACCTTGGAGC	ATCTCATCTG	TTACAGCTTC	CAAGTGGCTA	AGGGCATGGA	GTTCTTGGCA	3060
	TCGCGAAAGT	GTATCCACAG	GGACCTGGCG	GCACGAAATA	TCCTCTTATC	GGAGAAGAAC	3120
50	GTGGTTAAAA	TCTGTGACTT	TGGCTTGGCC	CGGGATATTT	ATAAAGATCC	AGATTATGTC	3180
	AGAAAAGGAG	ATGCTCGCCT	CCCTTTGAAA	TGGATGGCCC	CAGAAACAAT	TTTTGACAGA	3240
	GTGTACACAA	TCCAGAGTGA	CGTCTGGTCT	TTTGGTGTTC	TGCTGTGGGA	AATATTTTCC	3300
55	TTAGGTGCTT	CTCCATATCC	TGGGGTAAAG	ATTGATGAAG	AATTTTGTAG	GCGATTGAAA	3360
	GAAGGAACCT	GAATGAGGGC	CCCTGATTAT	ACTACACCAG	AAATGTACCA	GACCATGCTG	3420

GACTGCTGGC ACGGGGAGCC CAGTCAGAGA CCCACGTTTT CAGAGTTGGT GGAACATTTG 3480  
 GGAAATCTCT TGCAAGCTAA TGCTCAGCAG GATGGCAAAG ACTACATTGT TCTTCCGATA 3540  
 5 TCAGAGACTT TGAGCATGGA AGAGGATTCT GGAATCTCTC TGCCTACCTC ACCTGTTTCC 3600  
 TGTATGGAGG AGGAGGAAGT ATGTGACCCC AAATTCCATT ATGACAACAC AGCAGGAATC 3660  
 10 AGTCAGTATC TGCAGAACAG TAAGCGAAAG AGCCGGCCTG TGAGTGTAAG AACATTTGAA 3720  
 GATATCCCGT TAGAAGAACC AGAAGTAAAA GTAATCCCAG ATGACAACCA GACGGACAGT 3780  
 GGTATGGTTC TTGCCTCAGA AGAGCTGAAA ACTTTGGAAG ACAGAACCAA ATTATCTCCA 3840  
 15 TCTTTTGGTG GAATGGTGCC CAGCAAAAGC AGGGAGTCTG TGGCATCTGA AGGCTCAAAC 3900  
 CAGACAAGCG GCTACCAGTC CGGATATCAC TCCGATGACA CAGACACCAC CGTGTACTCC 3960  
 AGTGAGGAAG CAGAACTTTT AAAGCTGATA GAGATTGGAG TGCAAACCGG TAGCACAGCC 4020  
 20 CAGATTCTCC AGCCTGACTC GGGGACCACA CTGAGCTCTC CTCCTGTTTA A 4071

(2) INFORMATION FOR SEQ ID NO:2:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1356 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Ser Lys Val Leu Leu Ala Val Ala Leu Trp Leu Cys Val Glu  
 1 5 10 15  
 35 Thr Arg Ala Ala Ser Val Gly Leu Pro Ser Val Ser Leu Asp Leu Pro  
 20 25 30  
 40 Arg Leu Ser Ile Gln Lys Asp Ile Leu Thr Ile Lys Ala Asn Thr Thr  
 35 40 45  
 Leu Gln Ile Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro  
 50 55 60  
 45 Asn Asn Gln Ser Gly Ser Glu Gln Arg Val Glu Val Thr Glu Cys Ser  
 65 70 75 80  
 Asp Gly Leu Phe Cys Lys Thr Leu Thr Ile Pro Lys Val Ile Gly Asn  
 85 90 95  
 50 Asp Thr Gly Ala Tyr Lys Cys Phe Tyr Arg Glu Thr Asp Leu Ala Ser  
 100 105 110  
 Val Ile Tyr Val Tyr Val Gln Asp Tyr Arg Ser Pro Phe Ile Ala Ser  
 115 120 125  
 55 Val Ser Asp Gln His Gly Val Val Tyr Ile Thr Glu Asn Lys Asn Lys  
 130 135 140

Thr Val Val Ile Pro Cys Leu Gly Ser Ile Ser Asn Leu Asn Val Ser  
 145 150 155 160  
 5 Leu Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly Asn Arg  
 165 170 175  
 Ile Ser Trp Asp Ser Lys Lys Gly Phe Thr Ile Pro Ser Tyr Met Ile  
 180 185 190  
 10 Ser Tyr Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp Glu Ser  
 195 200 205  
 Tyr Gln Ser Ile Met Tyr Ile Val Val Val Val Gly Tyr Arg Ile Tyr  
 210 215 220  
 15 Asp Val Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu  
 225 230 235 240  
 20 Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile  
 245 250 255  
 Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu  
 260 265 270  
 25 Val Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe  
 275 280 285  
 30 Leu Ser Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu  
 290 295 300  
 Tyr Thr Cys Ala Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr  
 305 310 315 320  
 35 Phe Val Arg Val His Glu Lys Pro Phe Val Ala Phe Gly Ser Gly Met  
 325 330 335  
 Glu Ser Leu Val Glu Ala Thr Val Gly Glu Arg Val Arg Ile Pro Ala  
 340 345 350  
 40 Lys Tyr Leu Gly Tyr Pro Pro Pro Glu Ile Lys Trp Tyr Lys Asn Gly  
 355 360 365  
 45 Ile Pro Leu Glu Ser Asn His Thr Ile Lys Ala Gly His Val Leu Thr  
 370 375 380  
 Ile Met Glu Val Ser Glu Arg Asp Thr Gly Asn Tyr Thr Val Ile Leu  
 385 390 395 400  
 50 Thr Asn Pro Ile Ser Lys Glu Lys Gln Ser His Val Val Ser Leu Val  
 405 410 415  
 Val Tyr Val Pro Pro Gln Ile Gly Glu Lys Ser Leu Ile Ser Pro Val  
 420 425 430  
 55 Asp Ser Tyr Gln Tyr Gly Thr Thr Gln Thr Leu Thr Cys Thr Val Tyr  
 435 440 445

	Ala	Ile	Pro	Pro	Pro	His	His	Ile	His	Trp	Tyr	Trp	Gln	Leu	Glu	Glu	
	450						455					460					
5	Glu	Cys	Ala	Asn	Glu	Pro	Ser	Gln	Ala	Val	Ser	Val	Thr	Asn	Pro	Tyr	
	465					470					475					480	
	Pro	Cys	Glu	Glu	Trp	Arg	Ser	Val	Glu	Asp	Phe	Gln	Gly	Gly	Asn	Lys	
					485					490					495		
10	Ile	Glu	Val	Asn	Lys	Asn	Gln	Phe	Ala	Leu	Ile	Glu	Gly	Lys	Asn	Lys	
				500					505					510			
	Thr	Val	Ser	Thr	Leu	Val	Ile	Gln	Ala	Ala	Asn	Val	Ser	Ala	Leu	Tyr	
			515					520					525				
15	Lys	Cys	Glu	Ala	Val	Asn	Lys	Val	Gly	Arg	Gly	Glu	Arg	Val	Ile	Ser	
		530				535						540					
20	Phe	His	Val	Thr	Arg	Gly	Pro	Glu	Ile	Thr	Leu	Gln	Pro	Asp	Met	Gln	
	545					550					555					560	
	Pro	Thr	Glu	Gln	Glu	Ser	Val	Ser	Leu	Trp	Cys	Thr	Ala	Asp	Arg	Ser	
					565					570					575		
25	Thr	Phe	Glu	Asn	Leu	Thr	Trp	Tyr	Lys	Leu	Gly	Pro	Gln	Pro	Leu	Pro	
				580					585					590			
	Ile	His	Val	Gly	Glu	Leu	Pro	Thr	Pro	Val	Cys	Lys	Asn	Leu	Asp	Thr	
			595					600					605				
30	Leu	Trp	Lys	Leu	Asn	Ala	Thr	Met	Phe	Ser	Asn	Ser	Thr	Asn	Asp	Ile	
		610					615					620					
	Leu	Ile	Met	Glu	Leu	Lys	Asn	Ala	Ser	Leu	Gln	Asp	Gln	Gly	Asp	Tyr	
35		625				630					635					640	
	Val	Cys	Leu	Ala	Gln	Asp	Arg	Lys	Thr	Lys	Lys	Arg	His	Cys	Val	Val	
					645					650					655		
40	Arg	Gln	Leu	Thr	Val	Leu	Glu	Arg	Val	Ala	Pro	Thr	Ile	Thr	Gly	Asn	
				660					665					670			
	Leu	Glu	Asn	Gln	Thr	Thr	Ser	Ile	Gly	Glu	Ser	Ile	Glu	Val	Ser	Cys	
			675					680					685				
45	Thr	Ala	Ser	Gly	Asn	Pro	Pro	Pro	Gln	Ile	Met	Trp	Phe	Lys	Asp	Asn	
		690				695						700					
	Glu	Thr	Leu	Val	Glu	Asp	Ser	Gly	Ile	Val	Leu	Lys	Asp	Gly	Asn	Arg	
50		705				710					715					720	
	Asn	Leu	Thr	Ile	Arg	Arg	Val	Arg	Lys	Glu	Asp	Glu	Gly	Leu	Tyr	Thr	
					725					730					735		
55	Cys	Gln	Ala	Cys	Ser	Val	Leu	Gly	Cys	Ala	Lys	Val	Glu	Ala	Phe	Phe	
				740					745					750			

	Ile Ile Glu Gly Ala Gln Glu Lys Thr Asn Leu Glu Ile Ile Ile Leu	755	760	765
5	Val Gly Thr Ala Val Ile Ala Met Phe Phe Trp Leu Leu Leu Val Ile	770	775	780
	Ile Leu Arg Thr Val Lys Arg Ala Asn Gly Gly Glu Leu Lys Thr Gly	785	790	795
10	Tyr Leu Ser Ile Val Met Asp Pro Asp Glu Leu Pro Leu Asp Glu His	805	810	815
	Cys Glu Arg Leu Pro Tyr Asp Ala Ser Lys Trp Glu Phe Pro Arg Asp	820	825	830
15	Arg Leu Lys Leu Gly Lys Pro Leu Gly Arg Gly Ala Phe Gly Gln Val	835	840	845
	Ile Glu Ala Asp Ala Phe Gly Ile Asp Lys Thr Ala Thr Cys Arg Thr	850	855	860
20	Val Ala Val Lys Met Leu Lys Glu Gly Ala Thr His Ser Glu His Arg	865	870	875
	Ala Leu Met Ser Glu Leu Lys Ile Leu Ile His Ile Gly His His Leu	885	890	895
	Asn Val Val Asn Leu Leu Gly Ala Cys Thr Lys Pro Gly Gly Pro Leu	900	905	910
30	Met Val Ile Val Glu Phe Cys Lys Phe Gly Asn Leu Ser Thr Tyr Leu	915	920	925
	Arg Ser Lys Arg Asn Glu Phe Val Pro Tyr Lys Thr Lys Gly Ala Arg	930	935	940
	Phe Arg Gln Gly Lys Asp Tyr Val Gly Ala Ile Pro Val Asp Leu Lys	945	950	955
40	Arg Arg Leu Asp Ser Ile Thr Ser Ser Gln Ser Ser Ala Ser Ser Gly	965	970	975
	Phe Val Glu Glu Lys Ser Leu Ser Asp Val Glu Glu Glu Glu Ala Pro	980	985	990
45	Glu Asp Leu Tyr Lys Asp Phe Leu Thr Leu Glu His Leu Ile Cys Tyr	995	1000	1005
	Ser Phe Gln Val Ala Lys Gly Met Glu Phe Leu Ala Ser Arg Lys Cys	1010	1015	1020
50	Ile His Arg Asp Leu Ala Ala Arg Asn Ile Leu Leu Ser Glu Lys Asn	1025	1030	1035
	Val Val Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Tyr Lys Asp	1045	1050	1055

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## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGAATTCCAT CCAAGCGGCA AATGTGTC

28

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGAATTCCGA GTCTTCTACA AGGGTCTC

28

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTATGACAAC ACAGCAGG

18

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

5 TTGGATCCTC GAGTTGGGGT GTGGATGC 28

(2) INFORMATION FOR SEQ ID NO:7:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

20 GGATCCAGAT GAACTCCCAT TG 22

(2) INFORMATION FOR SEQ ID NO:8:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 30 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

35 GTCGACTTAG TCTTTGCCAT CCTGCTGAGC 30

40